Efficient Techniques for Tree Similarity Queries[1]

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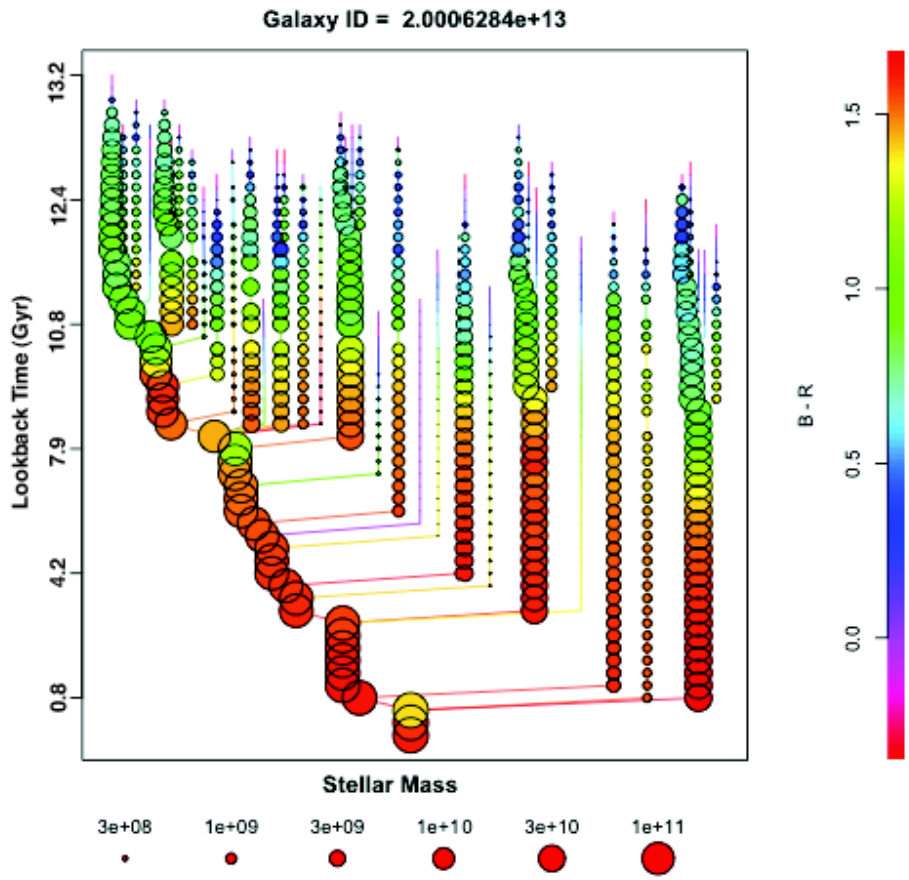
database research group

UNIVERSITY of SALZBURG

[1] Partially funded by Austrian Science Fund (FWF), FFTED Project P 29859

Trees Are Everywhere

- data formats (XML, JSON), directory hierarchies
- ERP: human resources, enterprise assets, bills of material
- NLP: syntax trees of natural languages
- software evolution: source code
- bioinformatics: RNA secondary structure, carbohydrates, neuronal morphology, phylogenetic trees
- image recognition: gesture and shape recognition
- astrophysics: ancestry trees of galaxies (merger trees)

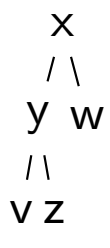
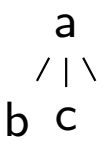
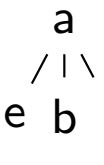


Source: `www.inspirehep.net`

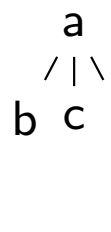
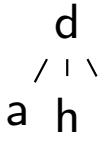
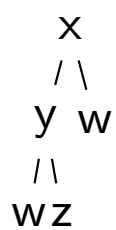
(19M trees, total of 750M nodes)

Similarity Join on Trees

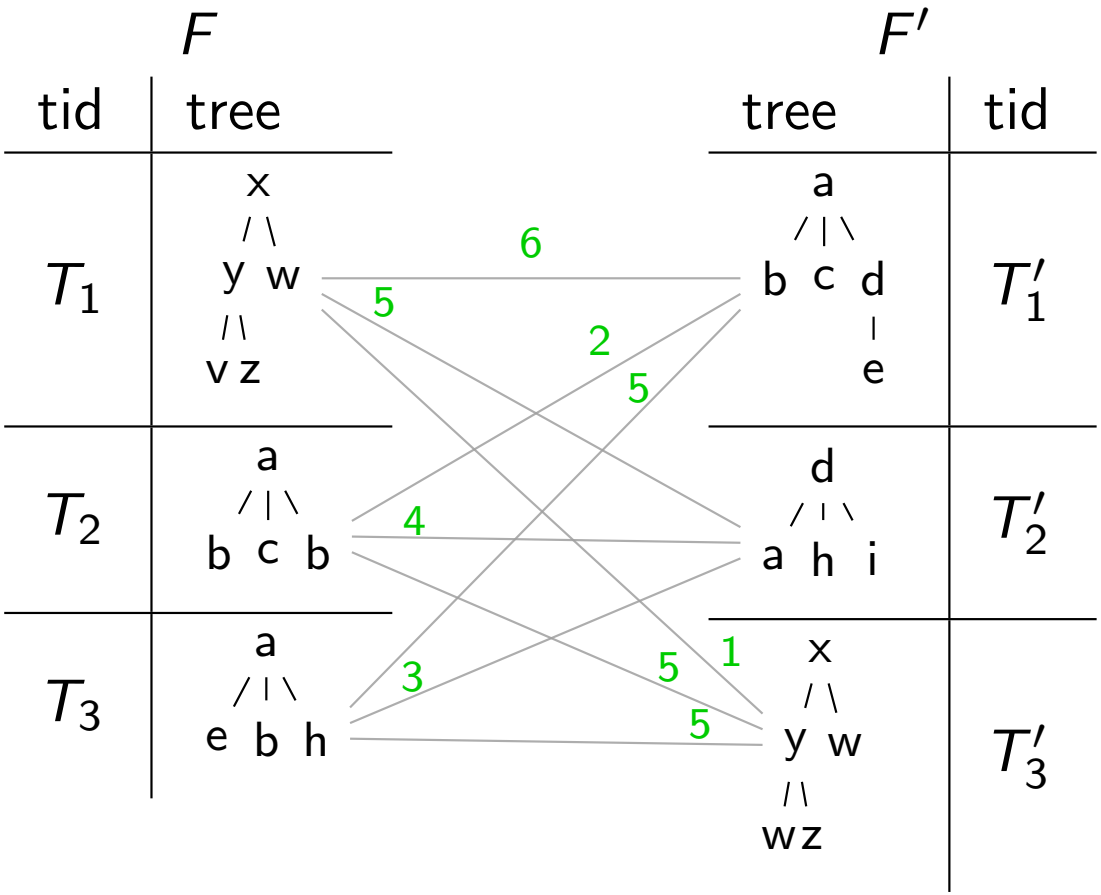
F

tid	tree
T_1	
T_2	
T_3	

F'

tree	tid
	T'_1
	T'_2
	T'_3

Similarity Join on Trees



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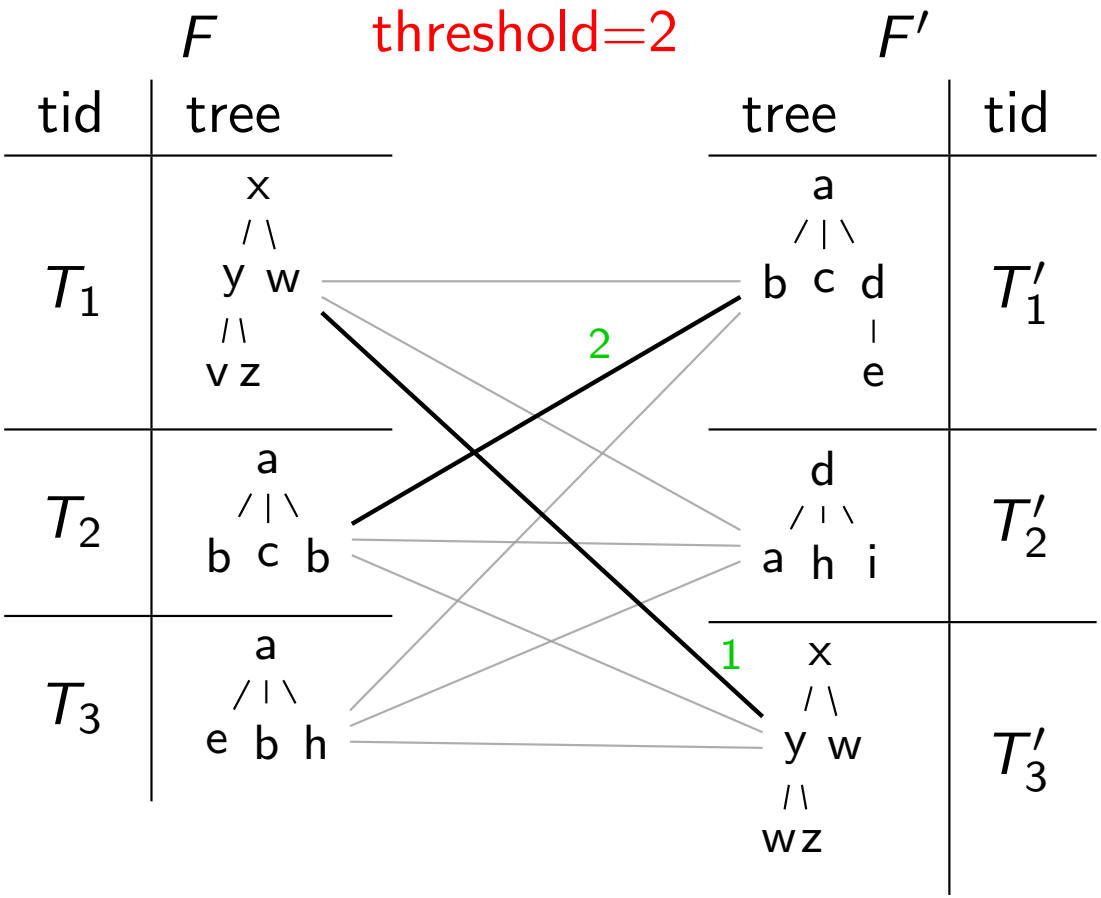

Outline

1. How similar are two trees?
2. From trees to integer sets
3. Avoiding the nested loop join

Outline

Tree Edit Distance (TED)

- minimum number of edit operations to transform one tree into another

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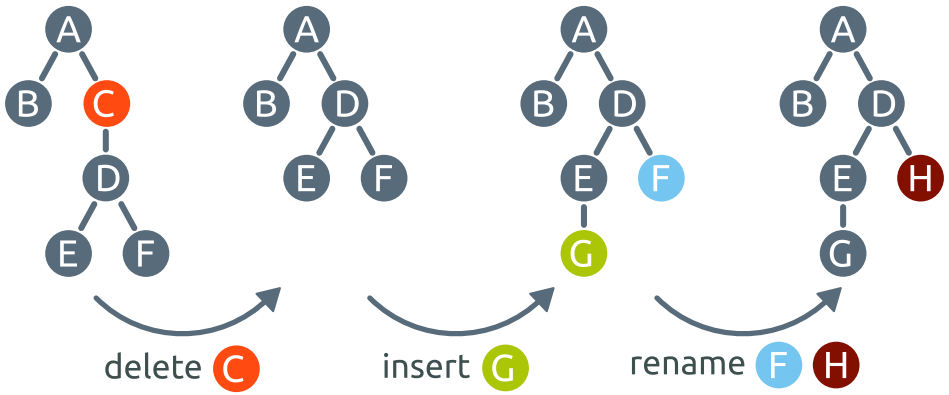

$$\text{TED} = 3$$

State of the Art in TED

Algorithm		Time	Space	Comments
Zhang&Shasha	1989	$O(n^4)$	$O(n^2)$	$O(n^2 \log^2 n)$ runtime for balanced trees
Demaine et al.	2009	$O(n^3)$	$O(n^2)$	worst case is frequent

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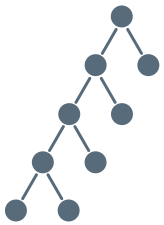

Zhang	0.5 sec
Demaine	30.9 sec

($\approx$ 1000 nodes)

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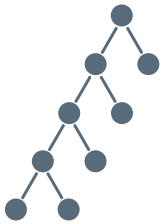

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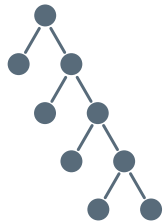

Zhang	247.6 sec
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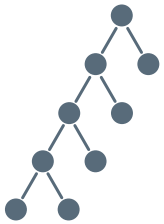

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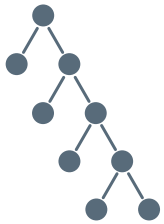

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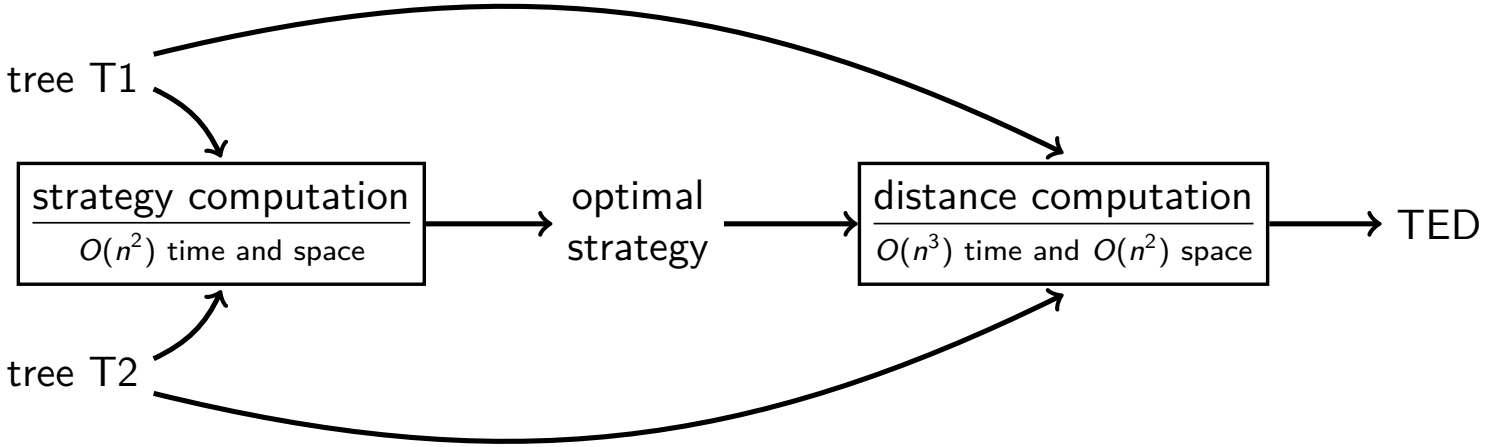
Problem: Hard-coded decomposition strategies

Robust Tree Edit Distance Algorithm (RTED)



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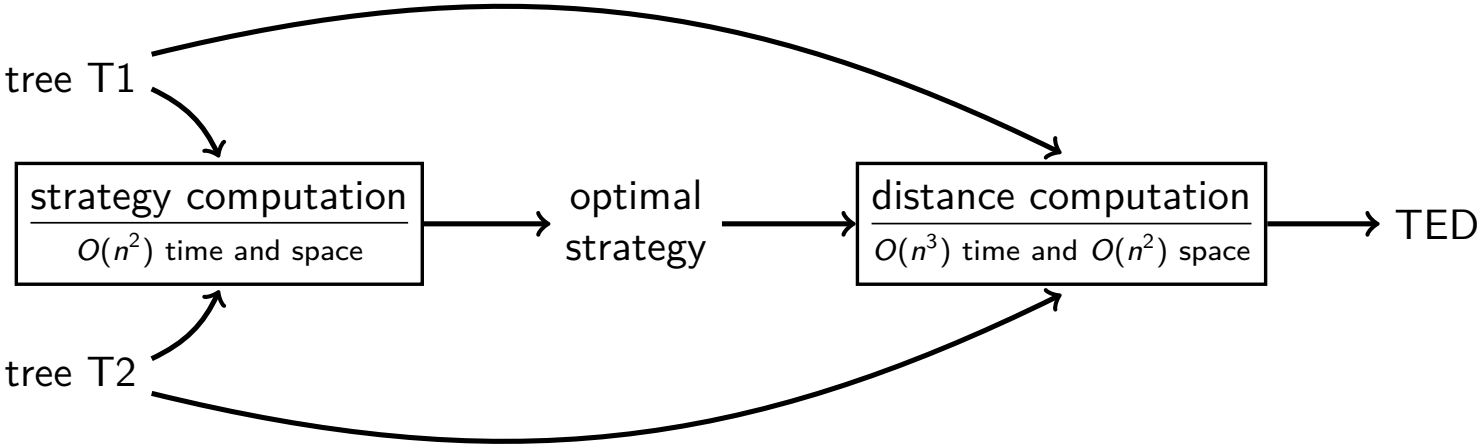

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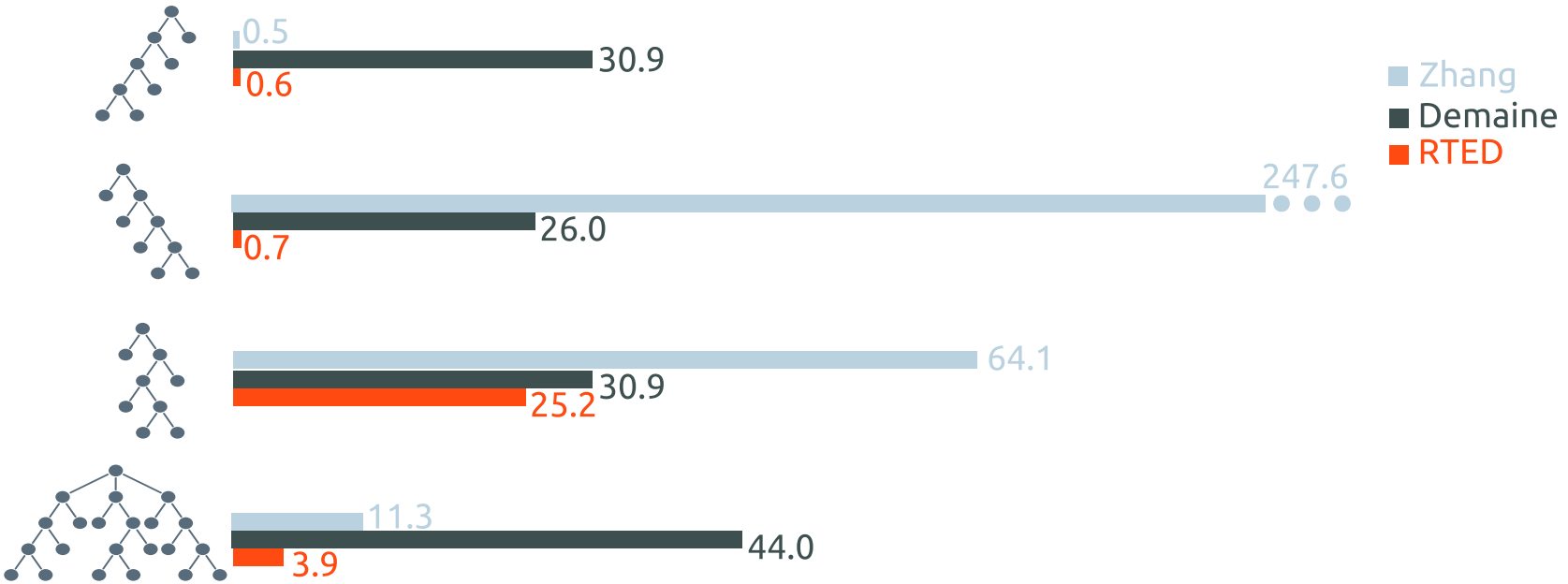
Pawlik&Augsten (RTED)	2011	$O(n^3)$	$O(n^2)$	optimal strategy

RTED: fastest known algorithm for TED.

Performance Evaluation

Runtime

- measure runtime (seconds)
- vary tree shape
- tree size $\approx$ 1000 nodes



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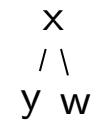
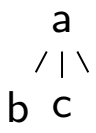
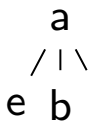
T_1	
T_2	
T_3	

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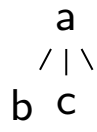
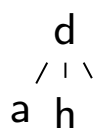
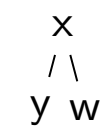
	T'_1
	T'_2
	T'_3

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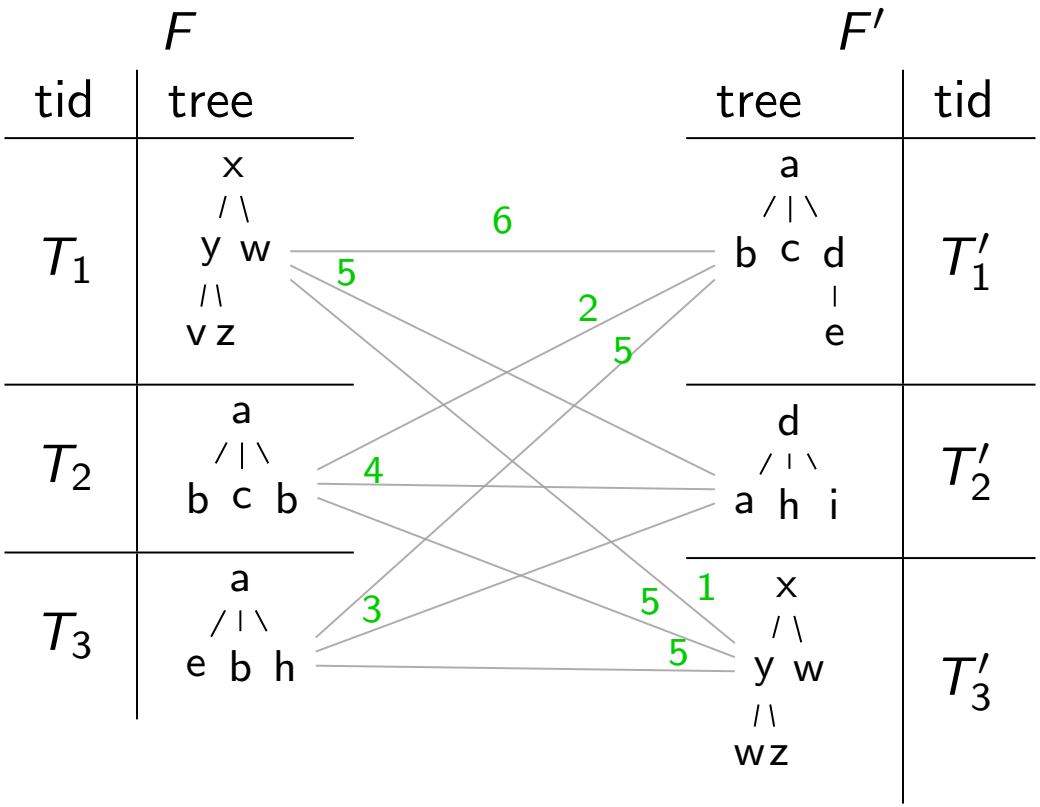
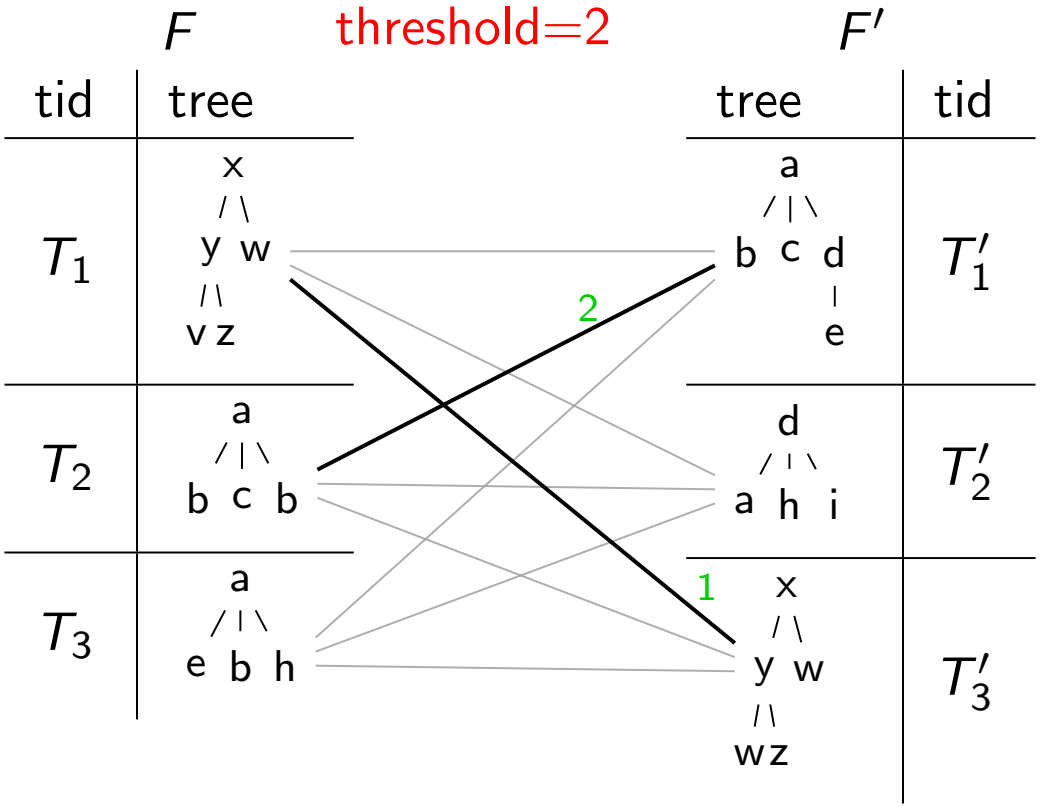


- Nested loop join (NLJ):
  1. compute distance between all pairs of trees

Similarity Join on Trees



- Nested loop join (NLJ):
  1. compute distance between all pairs of trees
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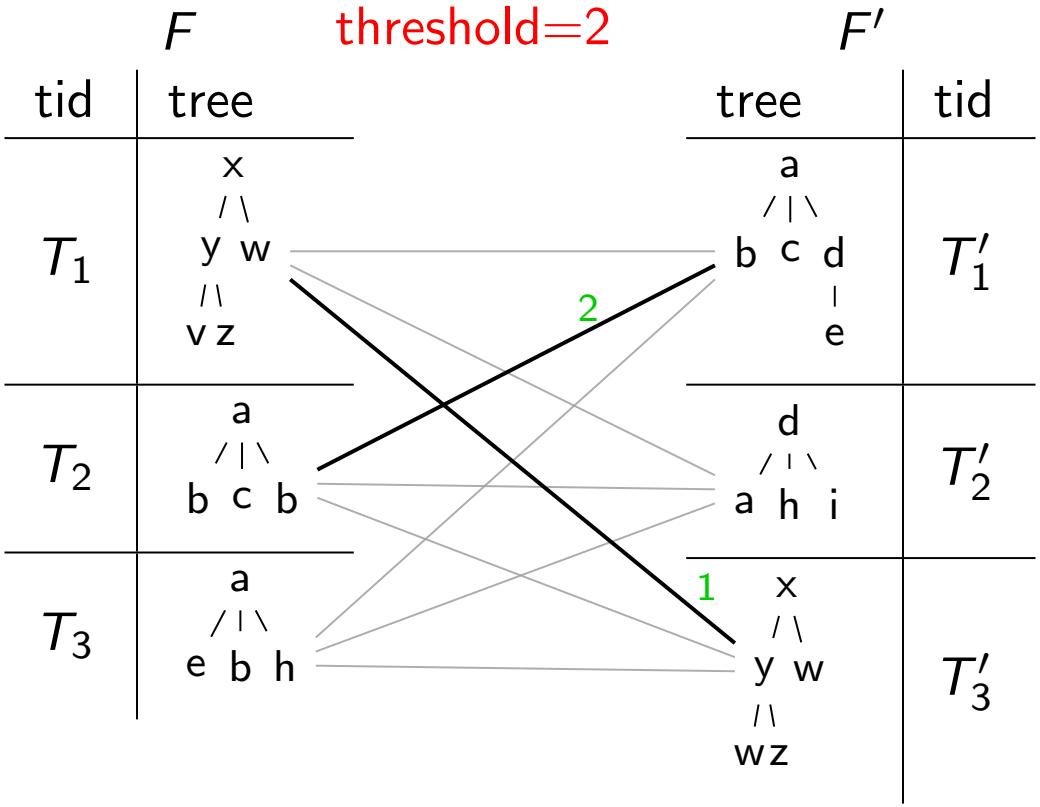

- Nested loop join (NLJ):
  1. compute distance between all pairs of trees
  2. return trees within threshold
- Very expensive: N^2 distance computations!

Standard Join Techniques Fail

- Sorting: Errors destroy sort order

customer

name	city
Frieda	Salzburg
Frodo	Auenland
Maria	Wien

customer

name	city
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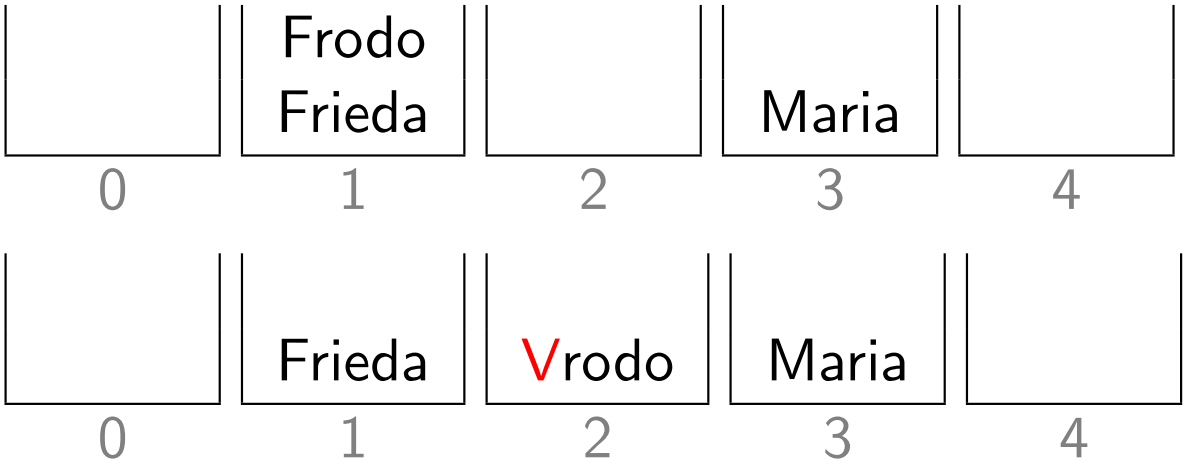
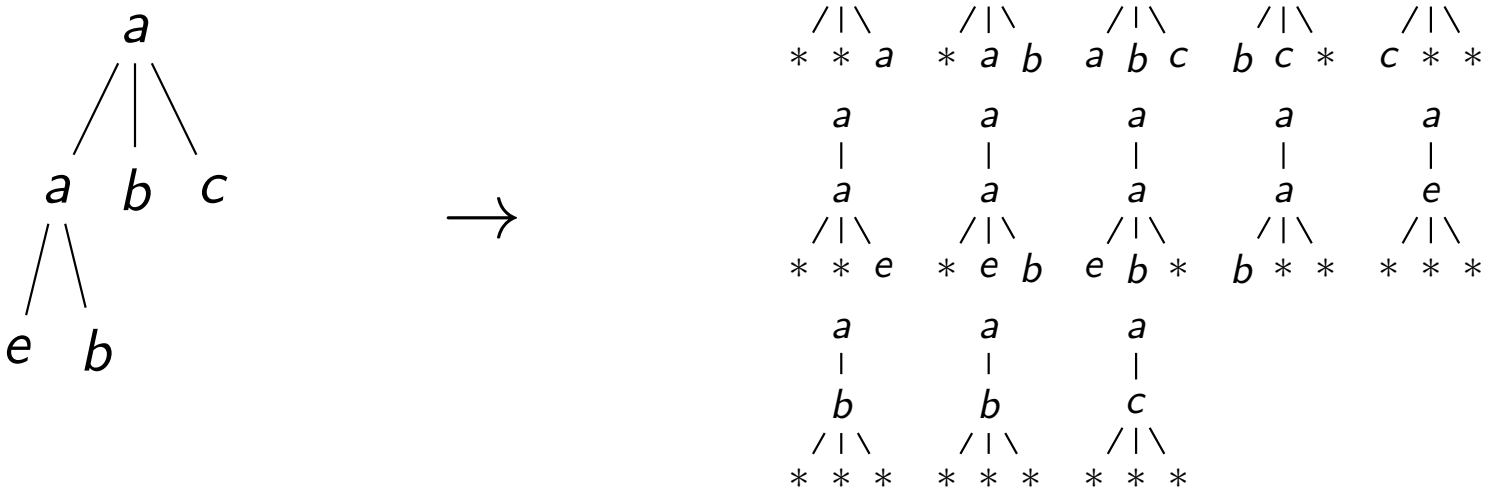
- Hashing: Errors change hash value



pq-Grams: From Trees to Sets

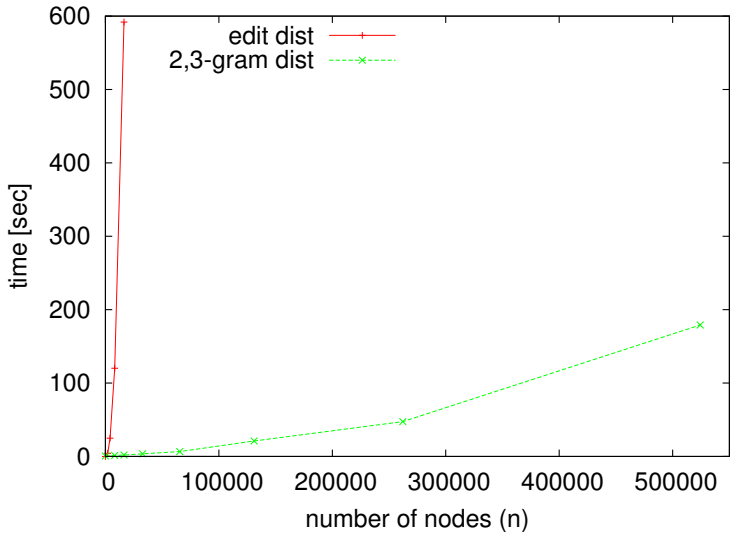
- Split trees into pq-Grams (small subtrees of fixed shape)



- Hash pq-grams to integers
- Intuition: Similar trees many common pq-grams

pq-Grams Have Useful Properties

- Efficiency
  - pq-gram runtime: $O(n \log n)$
  - edit distance runtime: $O(n^3)$
- Filter for edit distance
  - good approximation
  - guarantees **lower bound**
    (fanout weighting of operations)



Tree similarity simplified to set overlap.

Outline

Nested Loop Join for Sets – A Small Experiment

- Dataset: title and author of $n = 873k$ publications (DBLP)
  - avg. 15 words (min: 2, max: 289)
  - 409k different words, Zipfian frequency distribution

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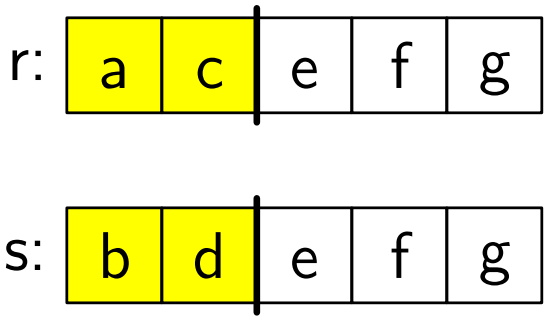
- Similarity check is very fast: 6 ns $\approx$ 15 CPU cycles
- Nested loop join: too many comparisons! (approx. 381 billion)

Overlap	0.95	0.9	0.8	0.7
Runtime [s]	2201	3136	4280	7770

NLJ does not even scale for very fast checks.

Trick: Avoid Touching Hopeless Candidates

- Prefix filter[1]: only look at small part of the set
  - sort sets and cut after prefix
  - no overlap in prefix $\Rightarrow$ similarity threshold not reachable

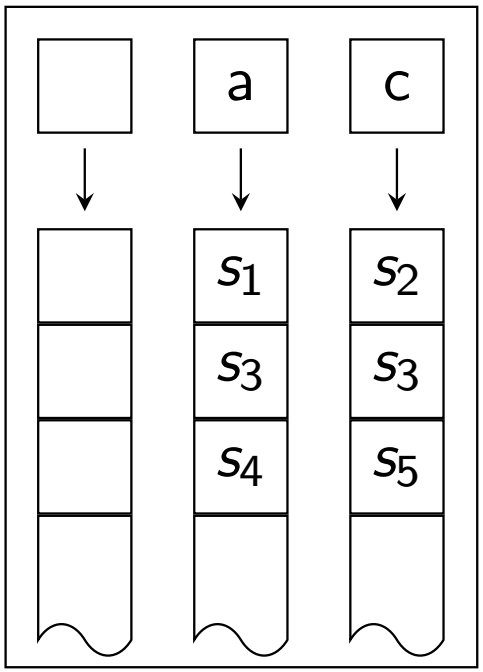


$$|r \cap s| \geq 4$$

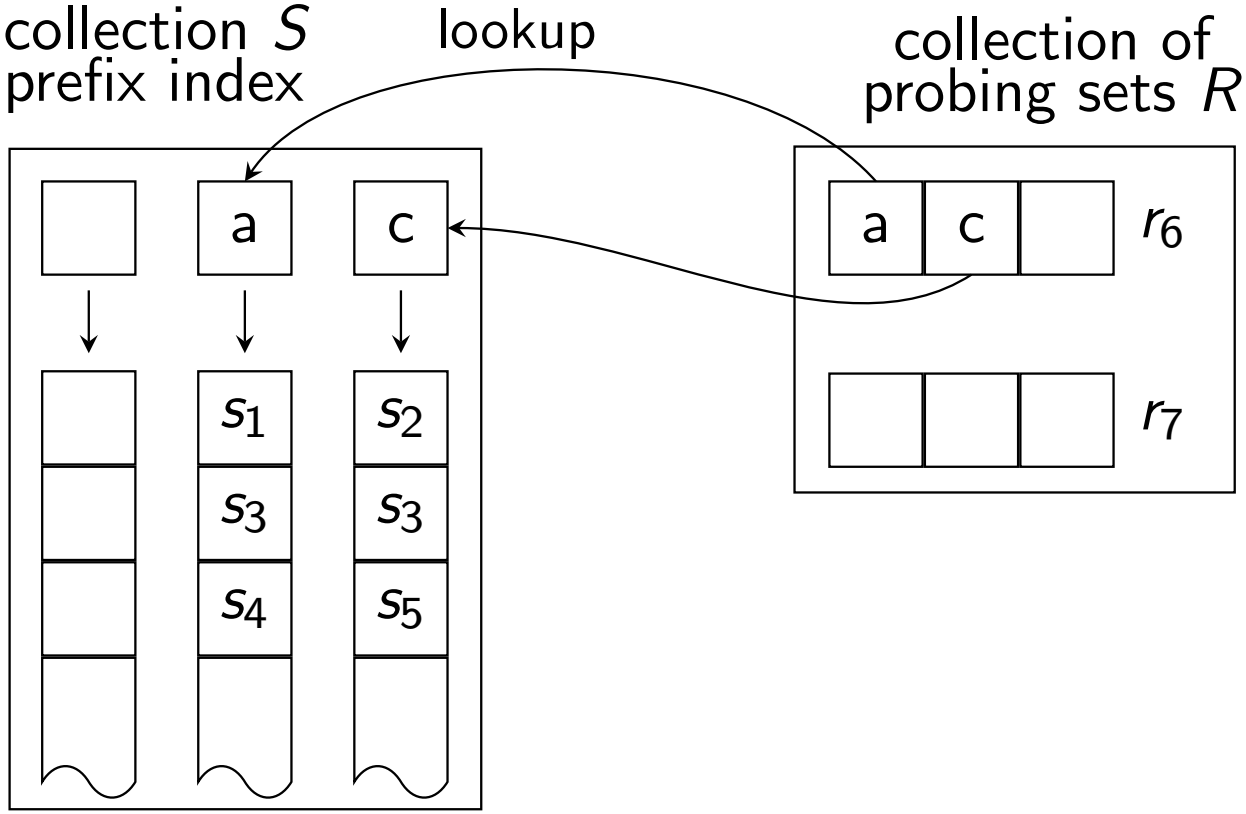
[1] Chaudhuri, Ganti, Kaushik. A primitive operator for similarity joins in data cleaning. ICDE 2006.

Prefix Index Join

collection S
prefix index



Prefix Index Join



Comparison to Nested Loop Join

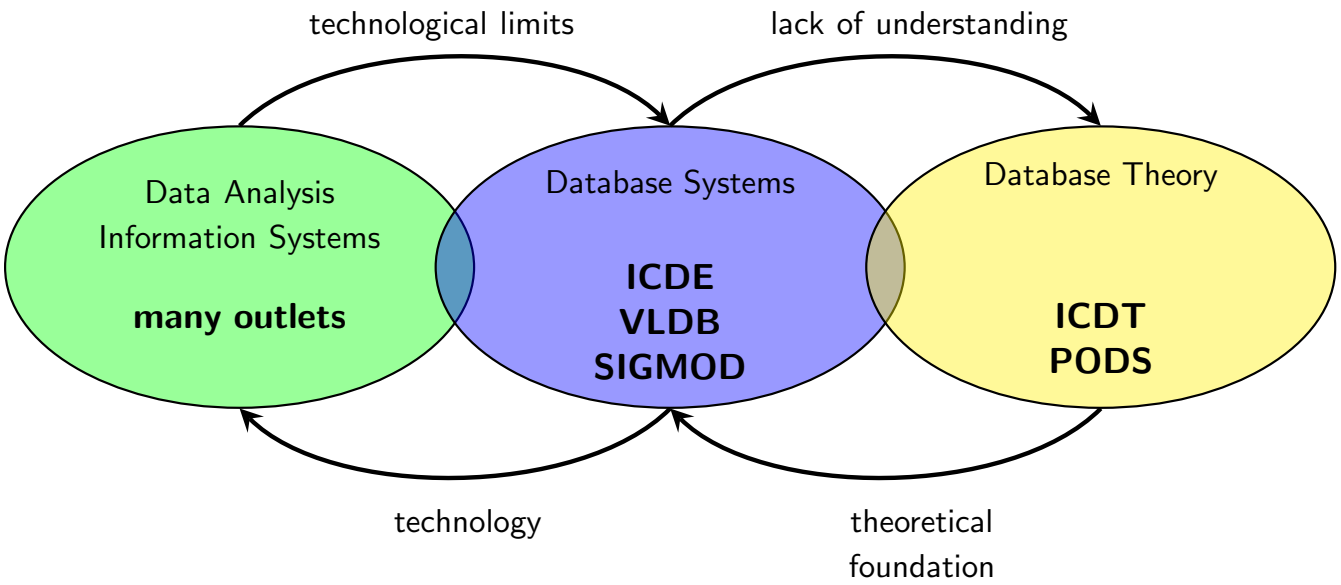
Overlap	Nested Loop Join	Prefix Join
0.95	2201 s	0.26 s
0.90	3136 s	0.44 s
0.80	4280 s	1.54 s
0.70	7770 s	4.93 s

Prefix Join 1500 to 8000 times faster than nested loop join!

Summary

- Set similarity join
  - RTED: efficient tree edit distance
  - pq-grams: from trees to sets
  - prefix: avoiding nested loop join
- Publications
  - Very Large Database Conference (VLDB 2005, 2011, 2016)
  - ACM Trans. on Database Systems (TODS 2010, 2015)
  - Elsevier Information Systems (Inf. Syst. 2016)
- Algorithms and technology matter
  - efficient solutions orders of magnitude faster

Conclusion and Outlook



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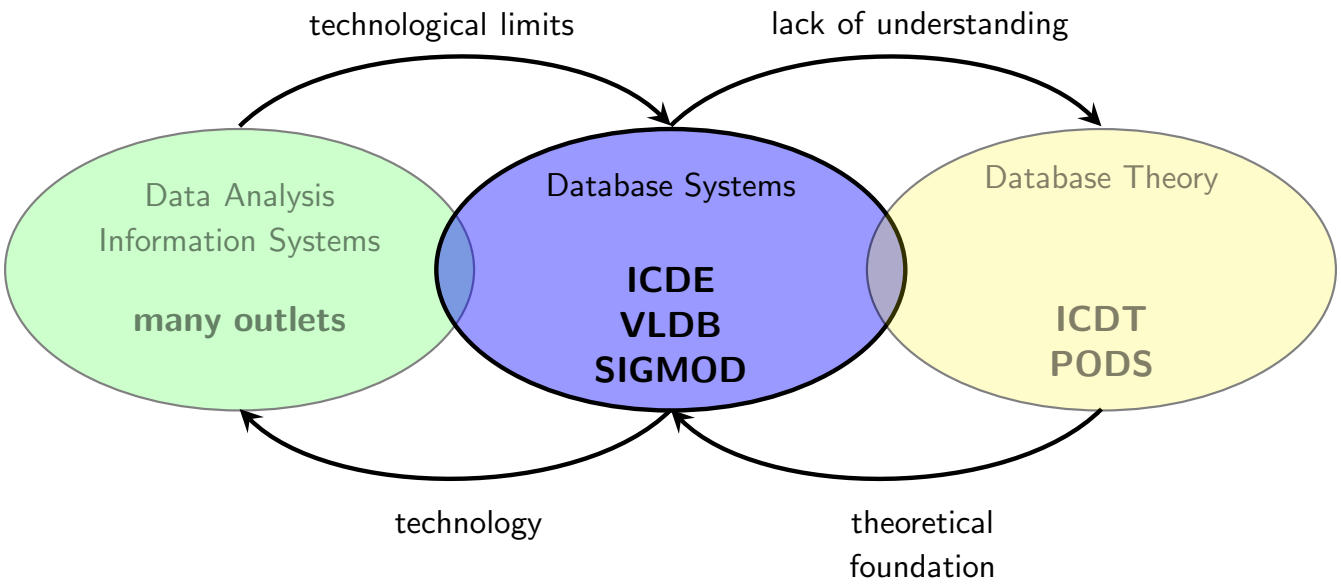

Efficient technology is key enabler for innovation in big data.

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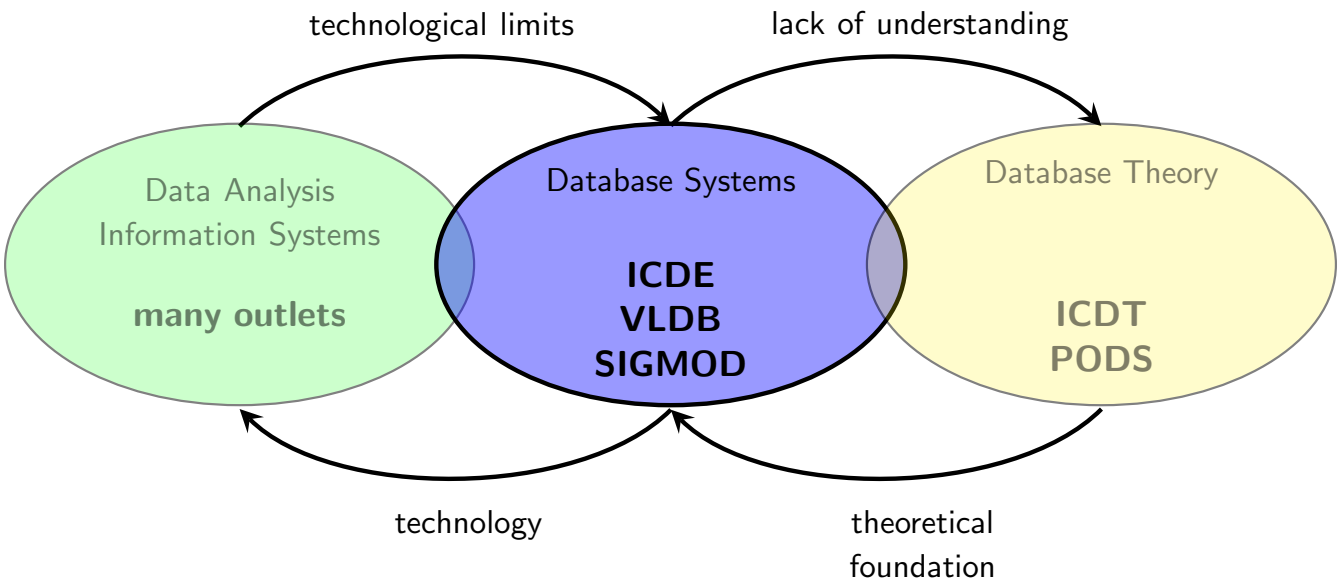

- DACH publications in top-3 DBS outlets: only 1.5% from Austria

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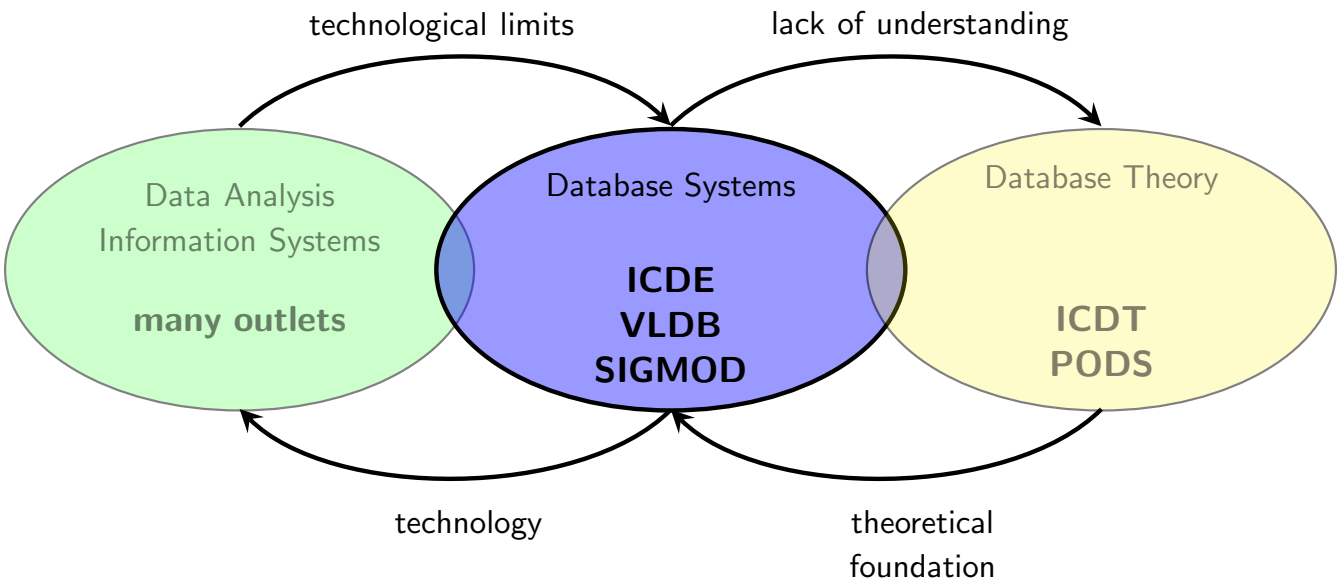

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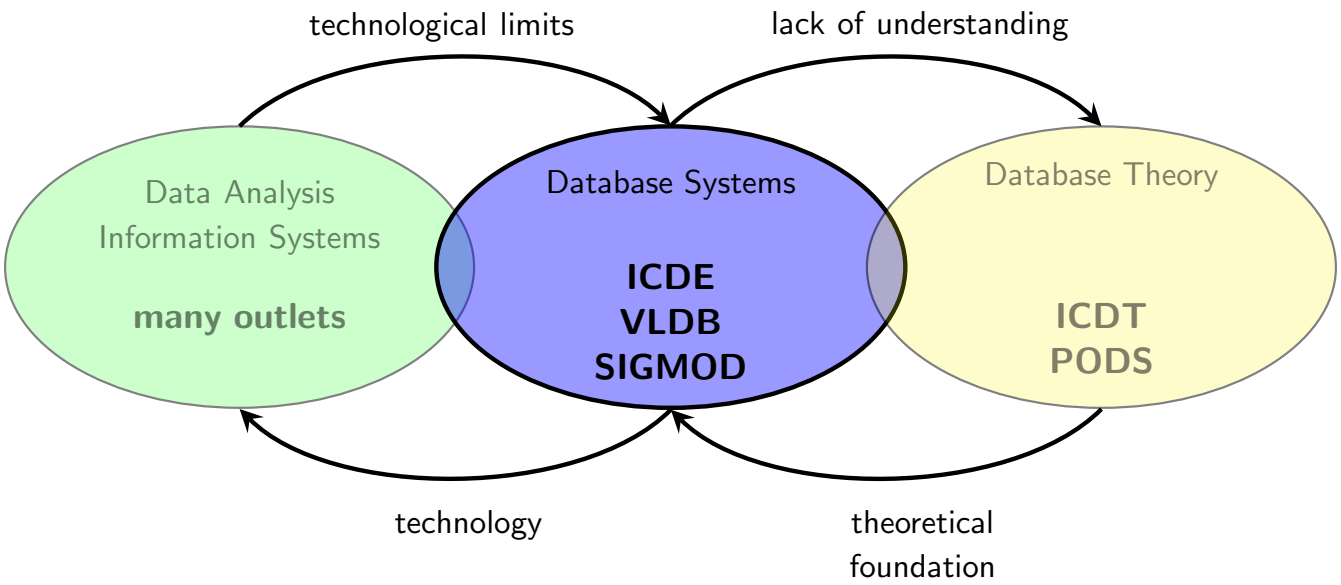

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- Master Data Science in Salzburg:
  data analysis + applications + technology
- Invitation: VLDB 2017 in Munich, EDBT 2018 in Vienna!

Efficient technology is key enabler for innovation in big data.

Thanks!

Thanks for your attention!

References I


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